



1/36

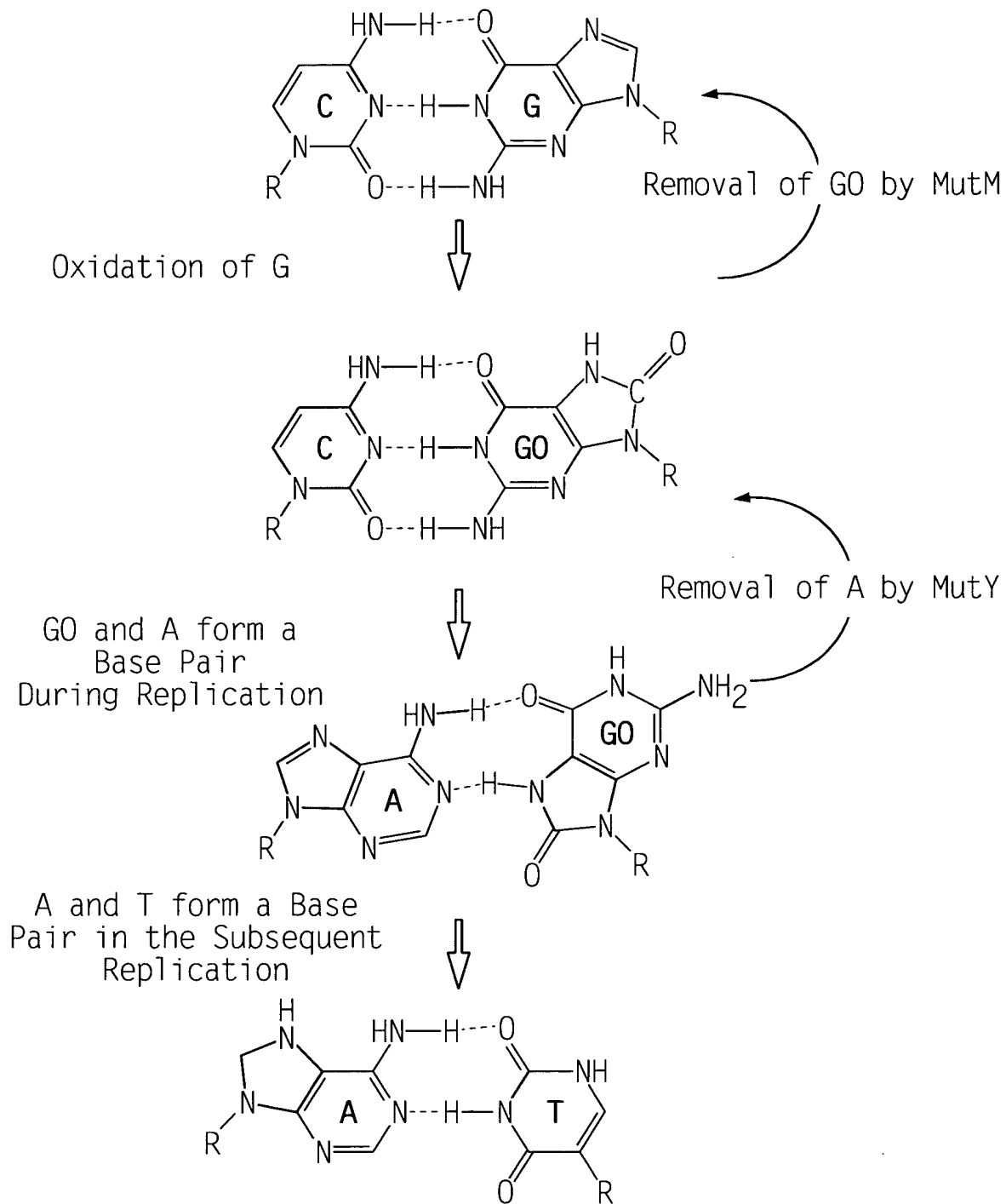


FIG. 1



2/36

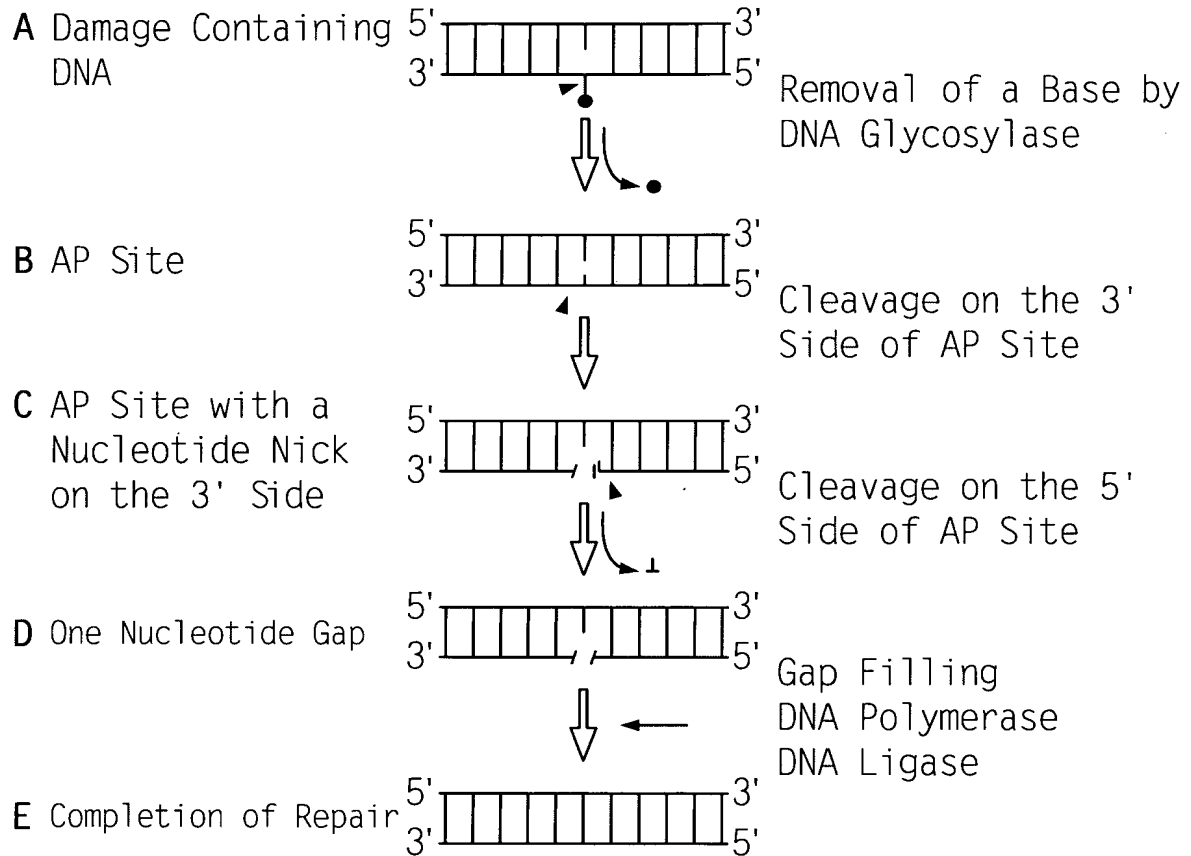


FIG. 2



3/36

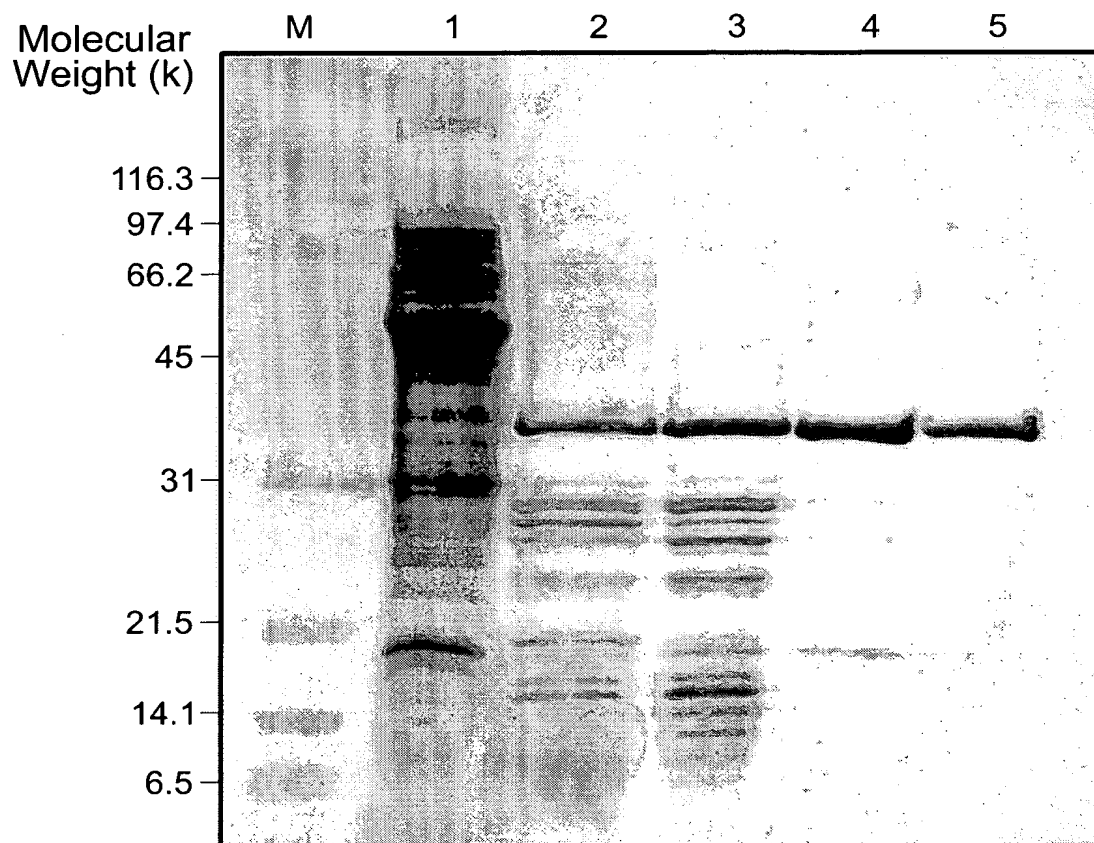


FIG. 3



4/36

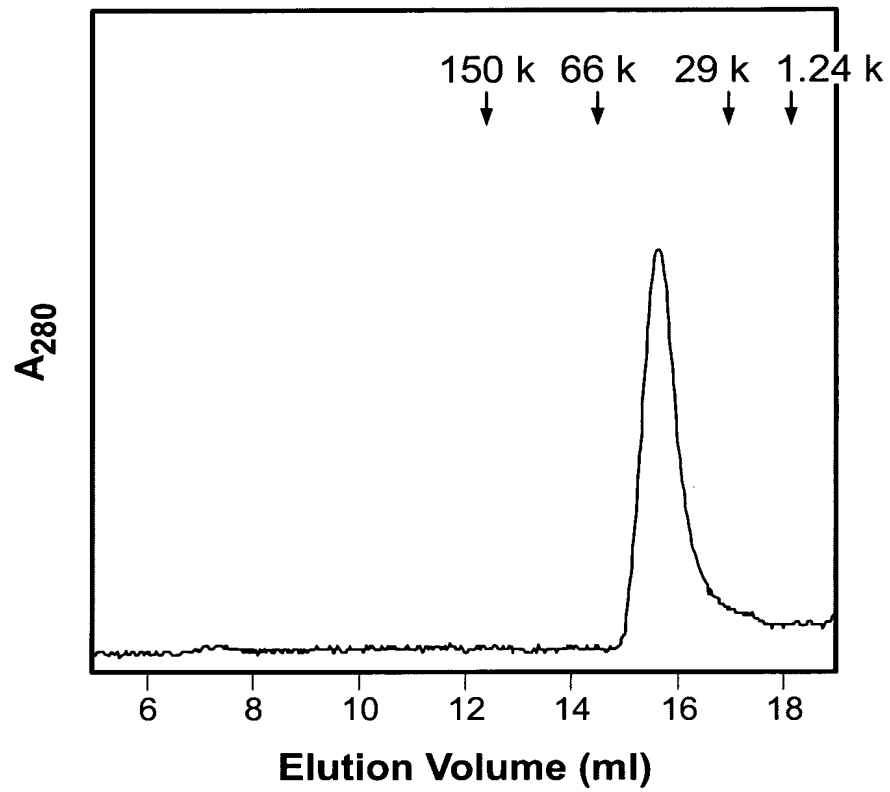


FIG. 4



5/36

Tth MutY	1	MEAWRKALAWREN-ARPLPWR-----GE-----KDPVRLVSEMLQOTRWEQALPIYRRFL	53
Hsa MutY	51	CDGLARQPEEVVLQASVSYHLFRDVAEVTAFRGLLSWDOE-KRDLPARRADEMDLD-----RRAYANWSEVMLQOTQWATVILNYITGMM	139
Spo MutY	1	MSDSNHFLDLHSYTQLEVERFRESIDFYDKT-KRIIPARKKECIPPSSEDSPLDWEOPVQRLYEMVSEMLQOTRWEITVKRYITKMM	88
Eco MutY	1	MQASQFSQAQLDWYKYGKTLPMQ-----ID-----KTPYKQMLSEVMLQOTQWATVILPIKFERFM	56
Eco EndoIII	1	MNKAKRELLRLREN--NPHPTT-----ELN-----FSSPFELLIAVLLSAQATDVSYNKATAKLY	55
Tth MutY	54	ERFPITIKALAAASIE-EVLRMQAGAYR-RAEH-HRLARSVEEL-----PPSFAELR-GPGPGPYTAAAVASTAFGERVAADVGNVRRVLSRLFRES	145
Hsa MutY	140	QKWPITLQDLASASLE-EVNQLMAGLYYS-RGRRLDEGARKVVEELGGHMPRTAEITLQQLPGMGRTYTAGAIASIAFGDATGVVDGNVARVLCRVRAIGA	237
Spo MutY	89	ETLPIIKSCAEAEYNTQWPLMSGMGFYT-RCKRLHQACQHLAKLHPSEIPRTGDEMAGKGPVGVPYTAGAVLSIAWKDPTGIVDGNVILRVLSRALAHHS	187
Eco MutY	57	ARFPITIDLANAPLD-EVLHLMTGLGYA-RARNLHKAACQVATLHGKFPETFEEMA-ALPGVGRSTAGAILSLGLKHFPITLDGNIKRVLCRCYAVSG	153
Eco EndoIII	56	PVANTPAAMLELGMF-GVKTYIKTIGLYNSKAENLIKTRILLEQHNGEVPEDRAALF-ALPGVGRKTAANVINTAFGWPTIATDTHIFRVCNRTQFAPG	153
Tth MutY	146	-PK-----EKELFWLAQGLPEGVDPGVWNOALMELGATVCLPKRRCGACPTLGAFCRG-----KEAPGRYP-----APR-----K	210
Hsa MutY	238	DPSSLVSOQLWGLAQQLMDP-ARPGDFNOAMELGATVCTPQRLCSQCPVFSLRARQVDEQQLASGSLSGSPDVEECAPNTGQCHLCLPPSEPMW	336
Spo MutY	188	DCSKGKANALLWKLANELMDP-VRPGDFNOALMELGALTCTPQSPRCSVCPTSEICKAYQ---EQNVIRDGNITIKYD--TEDVPCN-ICITDIPS---K	276
Eco MutY	154	MPGKKEVENKLWLSLSEQNTPA-VGVERFNOAMDLGAMICTRSKPKCSLCPUNGCTA-----AANNSWALYP-----GKK-----P	225
Eco EndoIII	154	-KN-----VEQMEKLLKWP-A-EFKVDCHHLLHGRYTCTARKPRCGSCTLEDLCEY-----GKK-----P-----K	205
Tth MutY	211	RRAK-----EER--LVALVLLGRKG-----VHLERLEGR-----FQGLGVDFPP-PEL-P-GREAFGVRS-----RP-----L	266
Hsa MutY	337	QTLGV---VNFPRKASRKPREESSATCVLEQPGA---LGAQILLVORPNSGLAGLMEFDSVTW-EPSELQQRKALLQELQRWAGP-----LPATHLRHL	425
Spo MutY	277	EDLQNWVARYPVHPAKTKQRE-ERALVWTFQKTOPSTKEKFFLLPKRPSAGLLAGLWDFPTIEFGQESMPKQMDAEFKSIAQWISNDSRSLIKKYQSR	375
Eco MutY	226	QTL-----PER---TGYFLLLOH-----EDEVLLACRPPSGLMGGLYCFDPFAD-EESJ---LRQWLACRQ-----I AADNL TQL	287
Eco EndoIII	206	--K-----EKVDI	
Tth MutY	267	GEVRHALLTHRLR-----VEVR-GALWEGEEDPWKRPP--LPKLMKXVLRKALP-----LAH-----AGVPLPDA	325
Hsa MutY	426	GEVWHIFSHIKLTYQVYGLALEGOTPVTTTPPGARMLTOEEFHATAAVSTAMKKVFRMYGGQDGTGCKGSRQSVSSCSRKPRMGQQVLDNFFRSHISIDAHSLNSAAQ	535
Spo MutY	376	GRYLHIFSHIRKTSHVFYAIAS---PDIVTINEDFFMISSDLEHVGMC-----ELGLKNVRALEIKRK-----VTLSN-----FKPKLTSARLVTKAEC	461
Eco MutY	288	TAFRHIFSHFHLD-----IIP---MMLPVSSFTGCMQD-----EGNALWNLNADP-PSVG-----LAADVER-----LLQQLRTGAPV	350

Tth (Thermus thermophilus HBB), Hsa (Homo sapiens), Spo (Schizosaccharomyces pombe), Eco (Escherichia coli)
Residue essential for N-glycosylase activity * Residues constituting an iron-sulfur cluster

FIG. 5



6/36

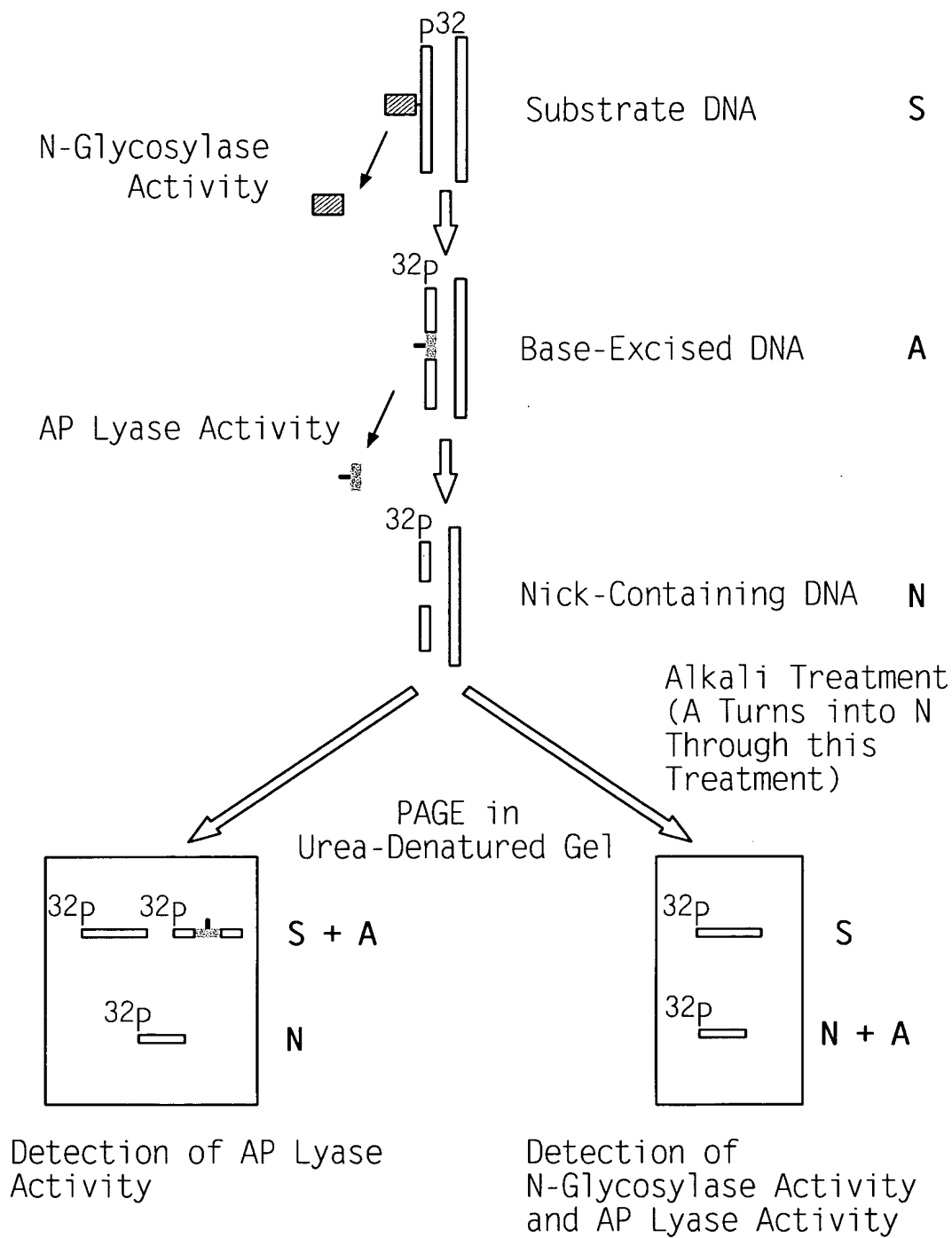


FIG. 6



7/36

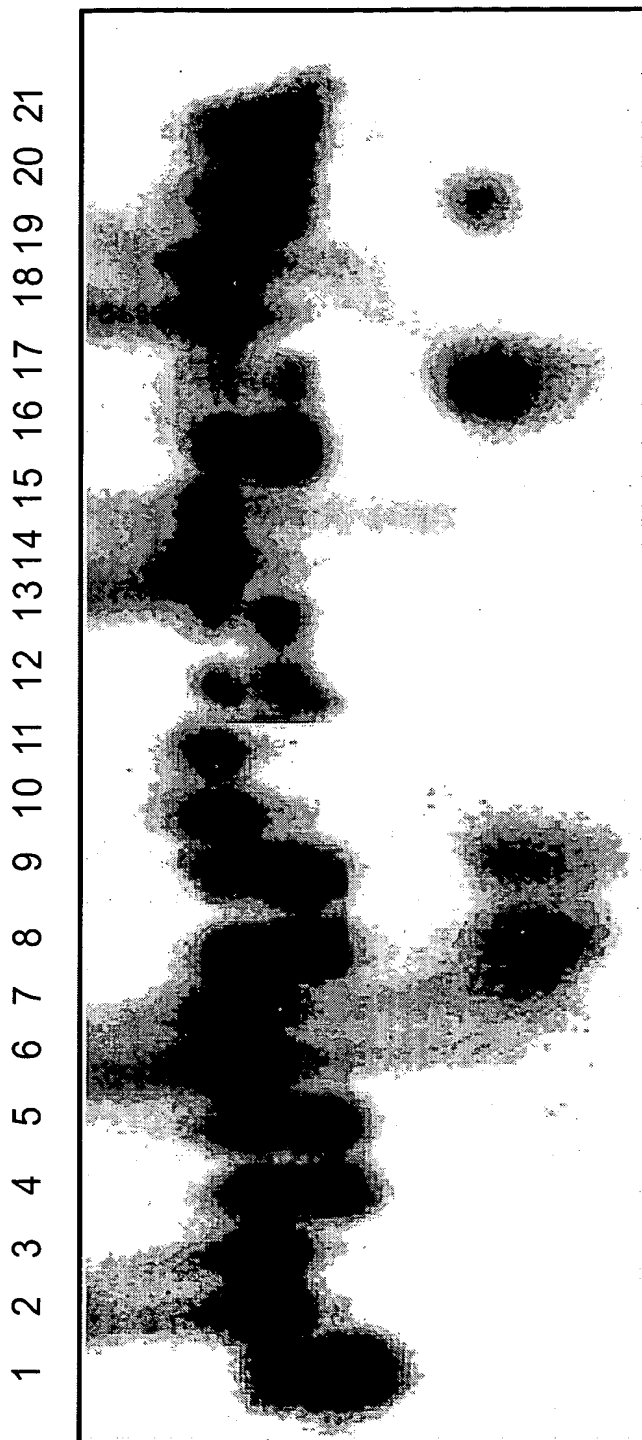
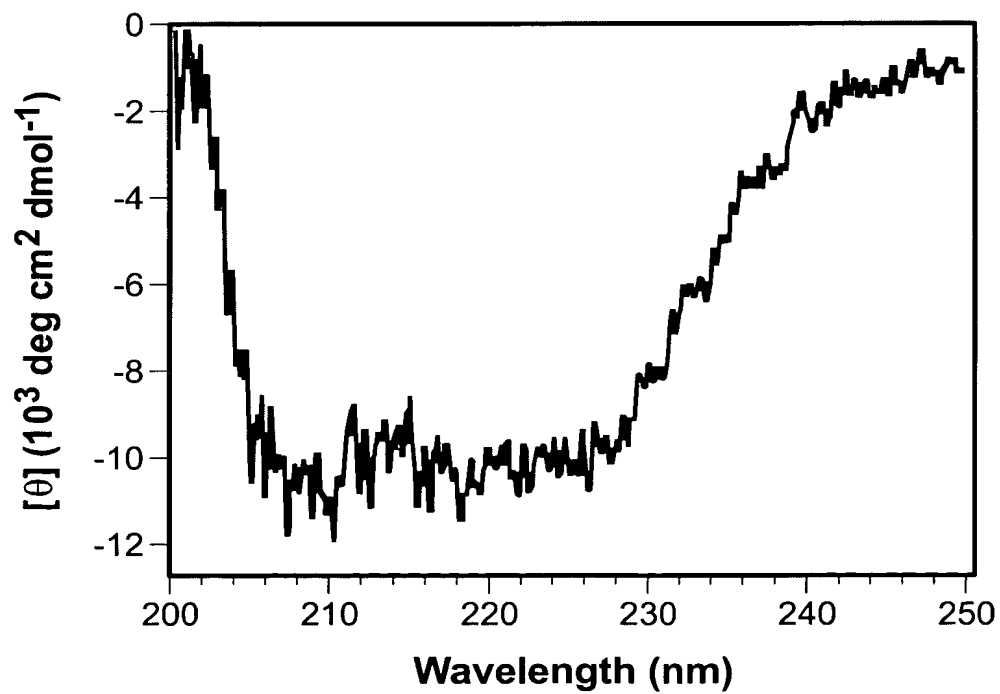
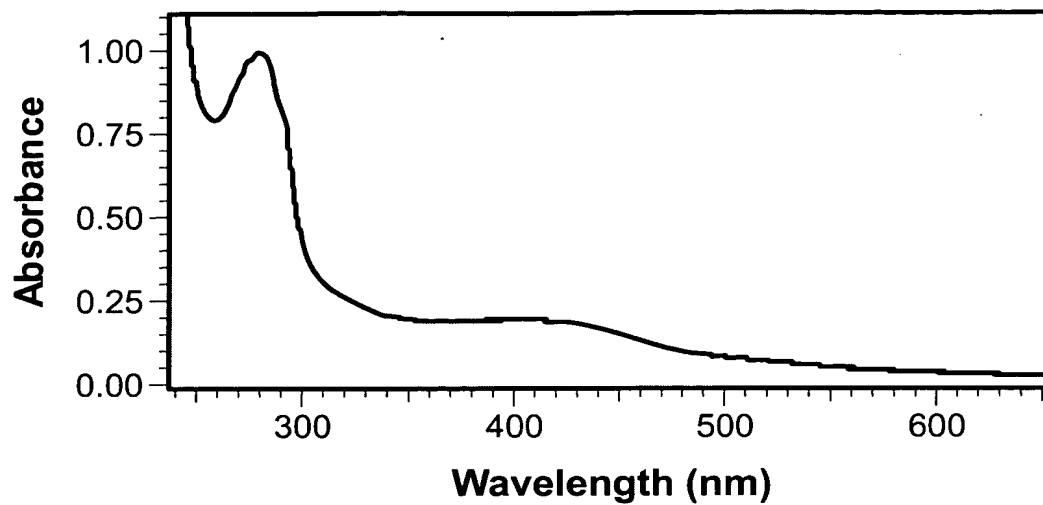


FIG. 7



8/36





9/36

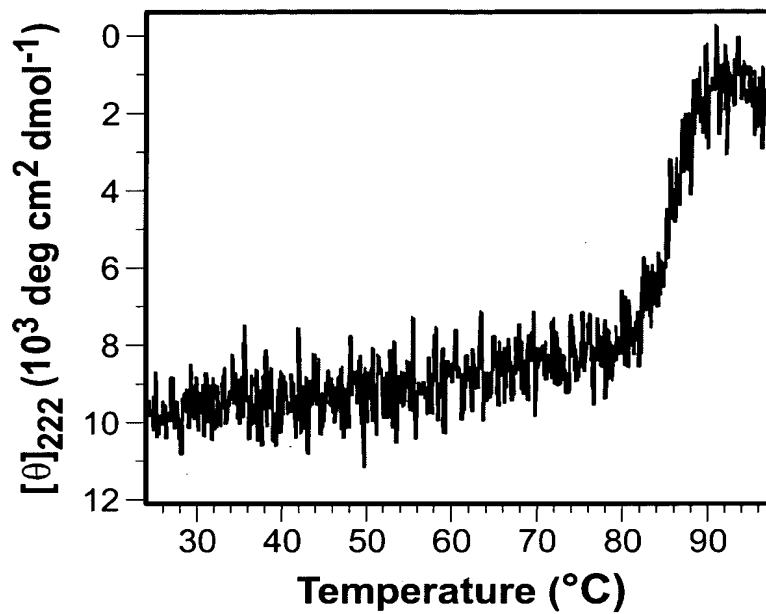


FIG. 10



10/36

5' - [³²P]AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG - 3'
3' - AATCTAGAACTGCCCCCTTXXGGCTTAAGCCGCTTGCACCGCTCTT - 5'

X : GO, G, C, T

Y : A, G



Annealing

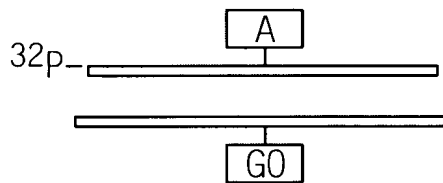
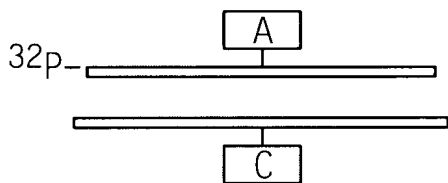
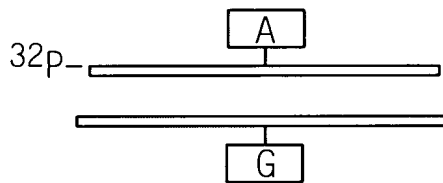
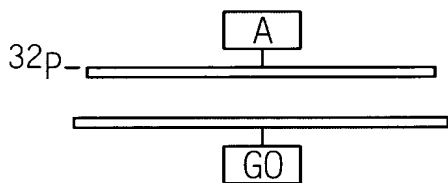


FIG. 11

11/36

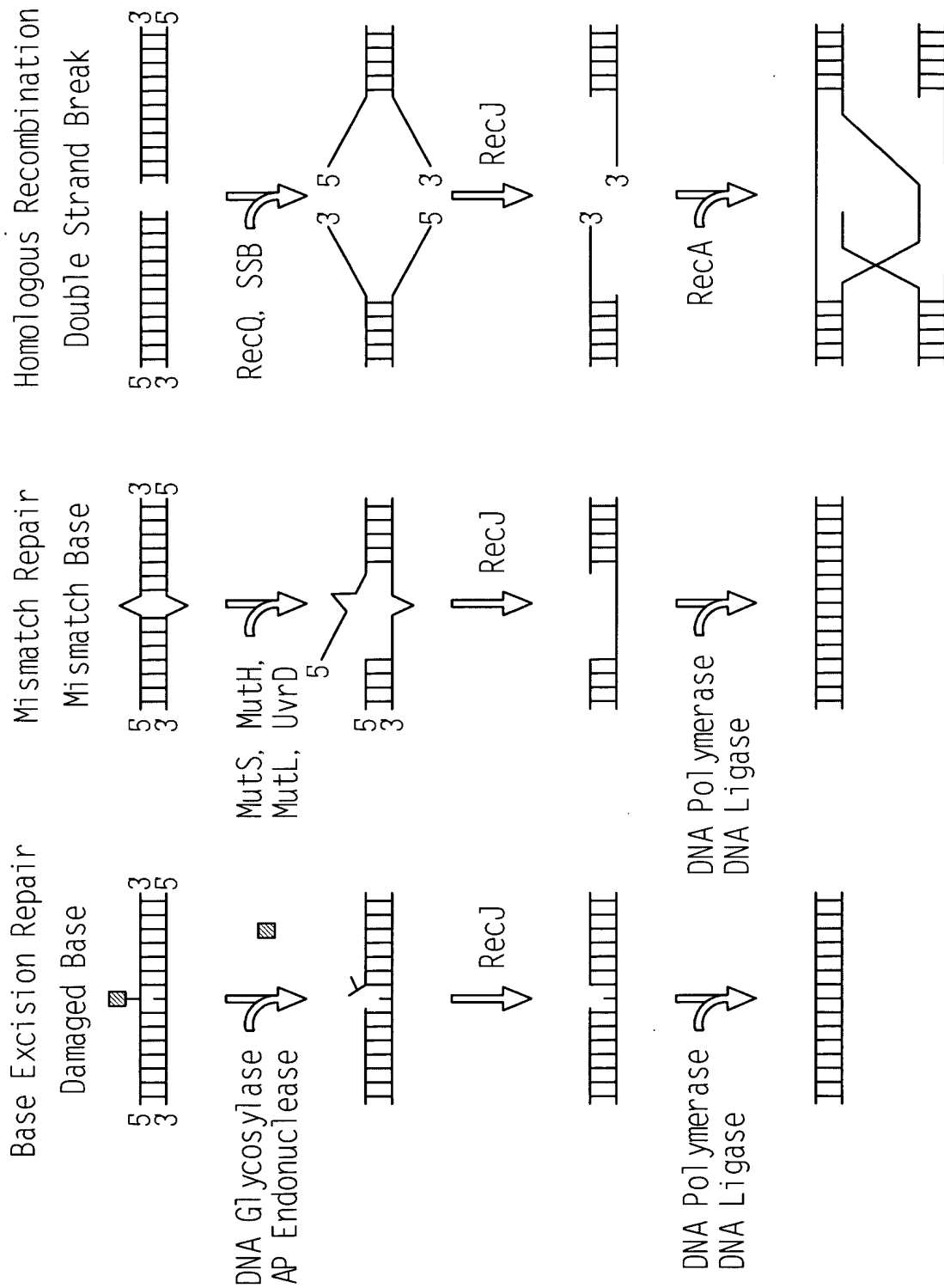


FIG. 12



12/36

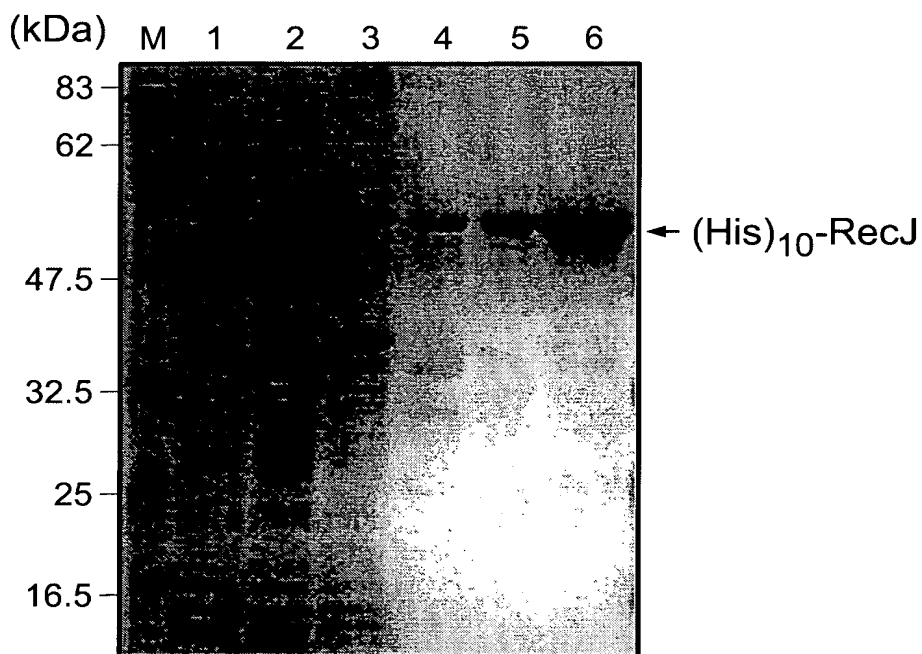


FIG. 13



13/36

Motif I			
RecJ_Tt	[73]	KRIRVHGDDADGLTGAILVRGLAALG	[100]
RecJ_Ec	[73]	TRIIIVVGDFDADGATSTALSVLAMRSLG	[100]
RecJ_Aa	[78]	KRIIIYGDYDVGITGTAILYRVLKLLG	[105]
RecJ_Hp	[47]	TEILVVGDDADGVISSAIMAKFFESLN	[74]
RecJ_Hi	[68]	QKIVIVGDFDADGATSTALSVLALRQLG	[95]
PPX1_Sc	[30]	TICVGNESADMDSTASAITTYSYCQYIYN	[57]
PRUNE_Dm	[37]	HLVMGNESCDLDSAVSAITLAFVYAASS	[60]
		Motif II	Motif III
RecJ_Tt	[129]	SDLFLITVDCGITNHAELRE	[147] [153] VEVIVTPPHTPGK [165]
RecJ_Ec	[131]	AQLIVTVONGISSHAGVEH	[49] [155] IPVIVTPPHLPGD [165]
RecJ_Aa	[133]	GDFLITVONGTSAVEEIDQ	[151] [154] LETVVIPPHNVPP [166]
RecJ_Hp	[102]	APLIITVONGINAFEAAARF	[120] [126] YTLIITPHHCLHH [138]
RecJ_Hi	[126]	VQLLMTVONGVSSFDGVAF	[144] [150] IRVLVTPPHLPPE [162]
PPX1_Sc	[120]	ELNSYLVNDNDTPKNLKNY	[138] [141] NVVGTIDHFFDLQ [153]
PRUNE_Dm	[88]	PLVCEMWDRCRARVALPRRY	[106] [129] NVTEILDHRLPED [141]
		Motif IV	Specific Motif
RecJ_Tt	[210]	YADLAANGTIADVAPLWG	[228] [386] DLLLRYGGHKEAAGFAM [402]
RecJ_Ec	[226]	LLDLVALGTADVVPDAN	[244] [422] GMMLKFGGHAMAAGLSL [438]
RecJ_Aa	[215]	FLDLVALGLADYMPVNPV	[233] [404] DMFLKWGGHOKAMGLTL [420]
RecJ_Hp	[189]	LLCLAGVATIADMPLTFF	[207] [372] SLLLGYGGHRCACGLSV [388]
RecJ_Hi	[219]	LLDLVALGTADVVPDQN	[237] [415] NMILKFGGHAMAAGLSI [431]
PPX1_Sc	[191]	IALLMGATLIDTSNMRRK	[209]
PRUNE_Dm	[183]	VAQLLHATVLDITNFAPA	[201]

Tt : Thermus thermophilus HB8. Ec : Escherichia coli. Aa : Aquifex aeolicus.
 Hp : Helicobacter pylori. Hi : Haemophilus influenzae Rd.
 Sc : Saccharomyces cerevisiae. Dm : Drosophila melanogaster

FIG. 14



14/36

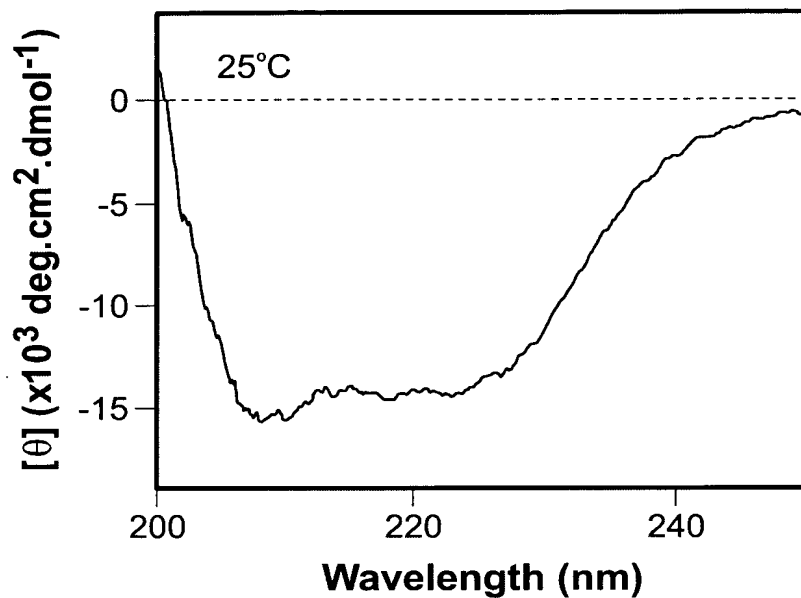


FIG. 15

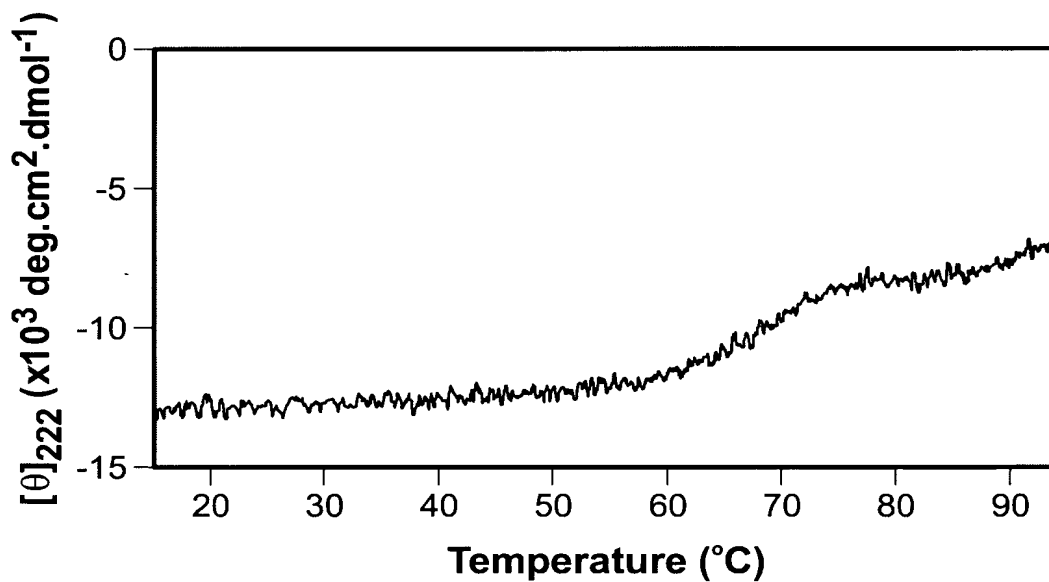


FIG. 16



15/36

Substrate DNA: 49' mer ssDNA

5' -ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'

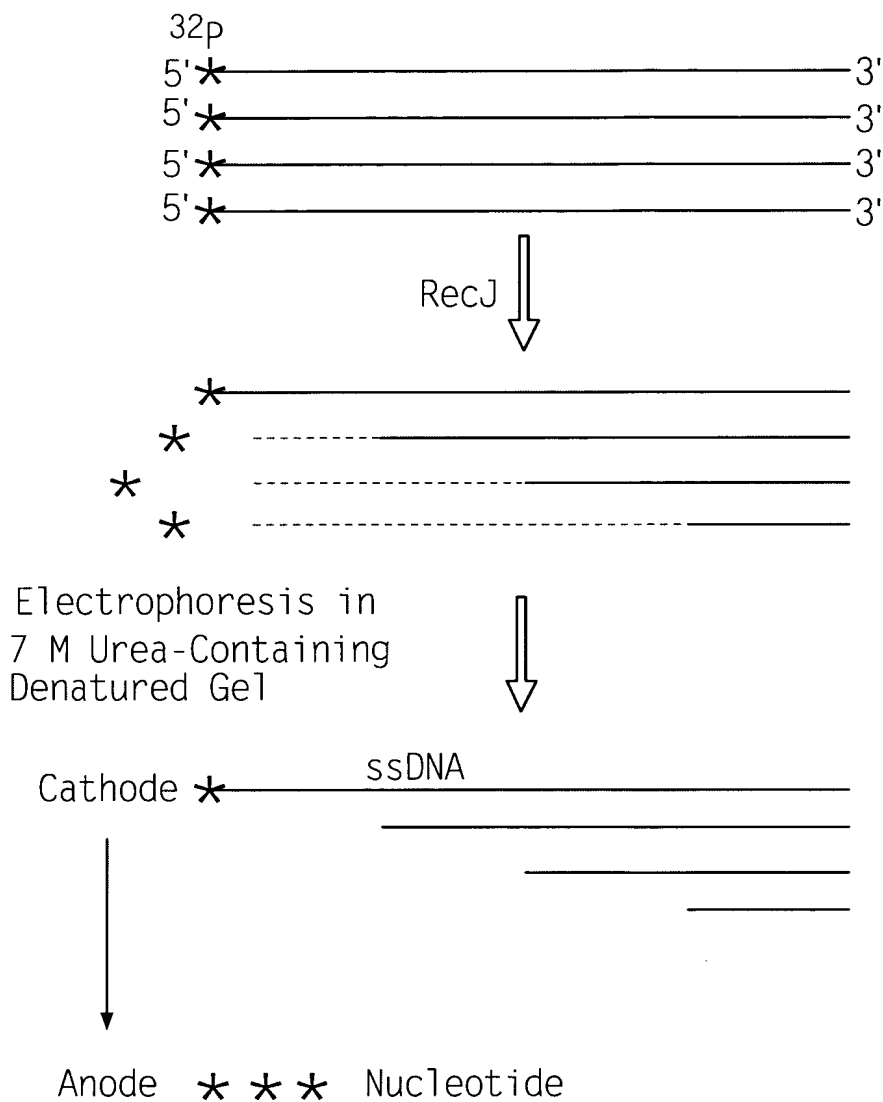


FIG.17



16/36

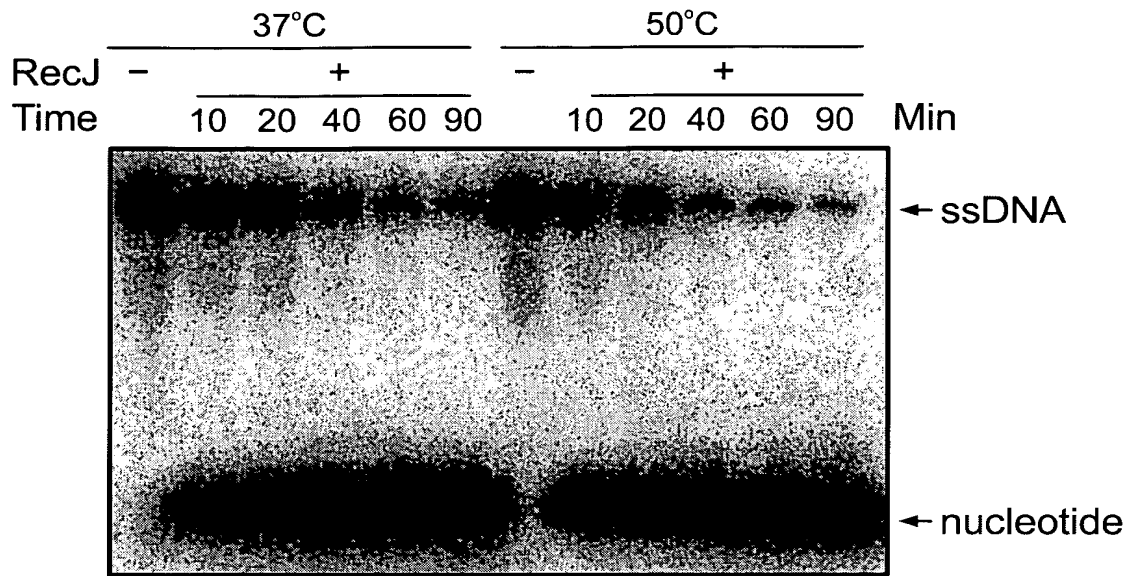


FIG. 18A

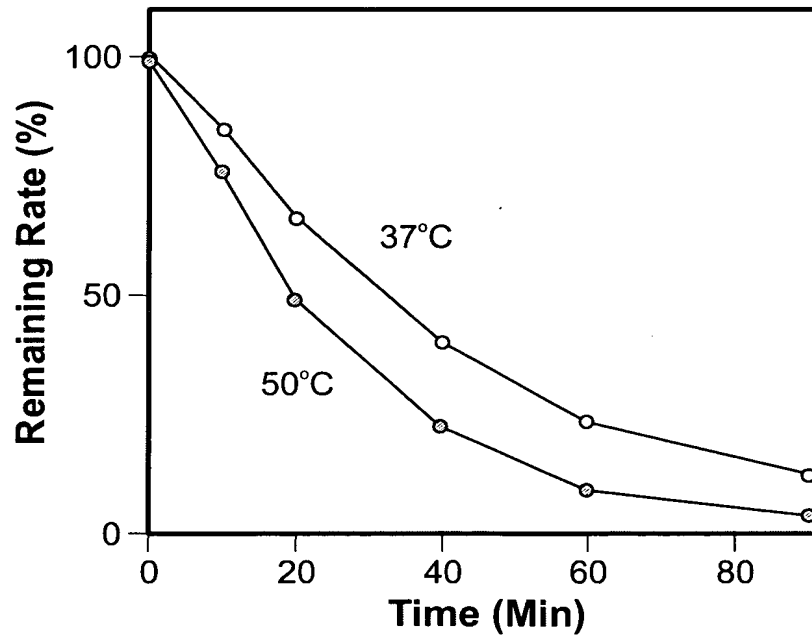


FIG. 18B



17/36

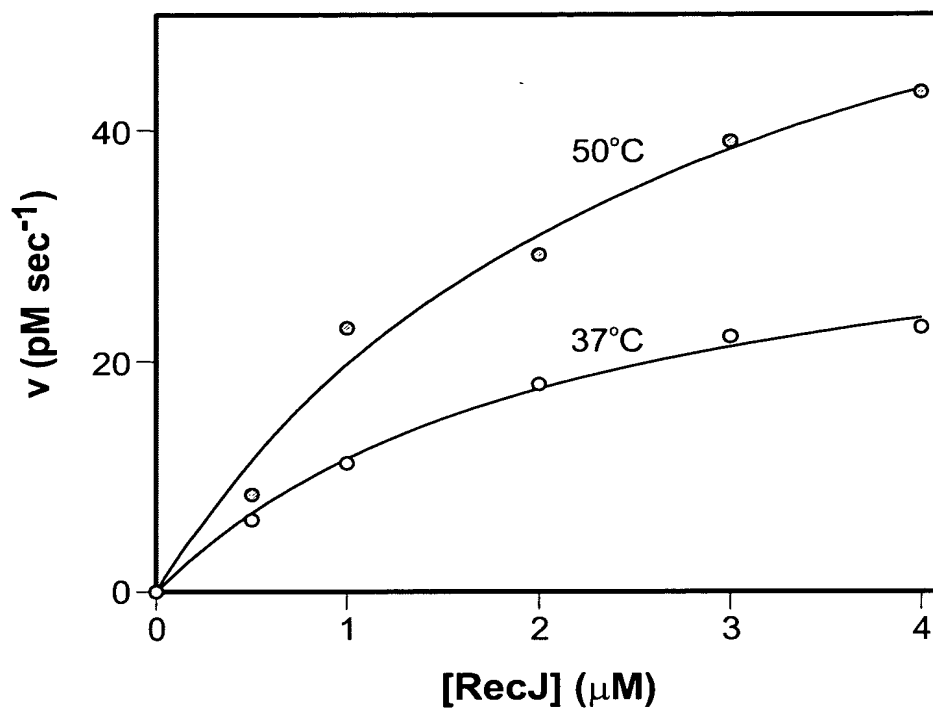


FIG. 19



18/36

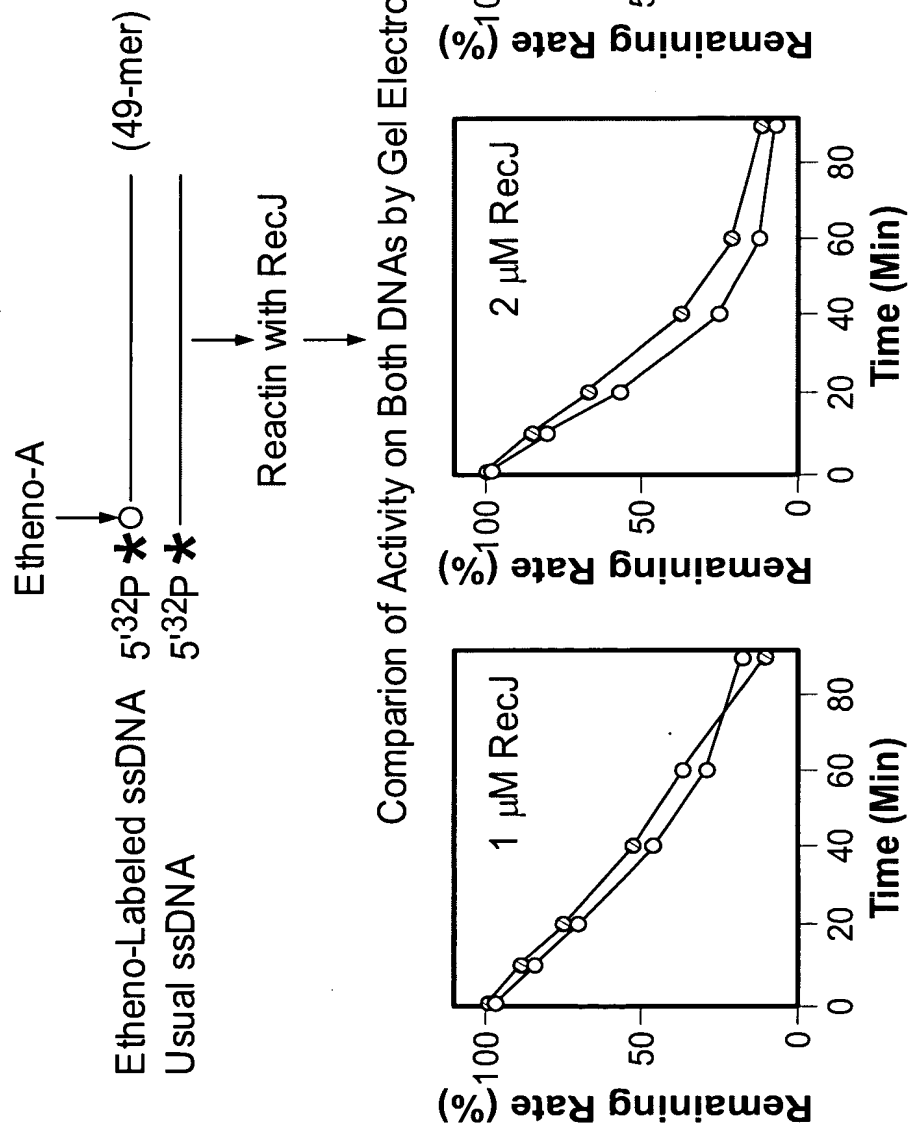


FIG. 20

19/36

**Substrate DNA : Etheno-Labeled Bovine Thymus
ssDNA (e DNA)**

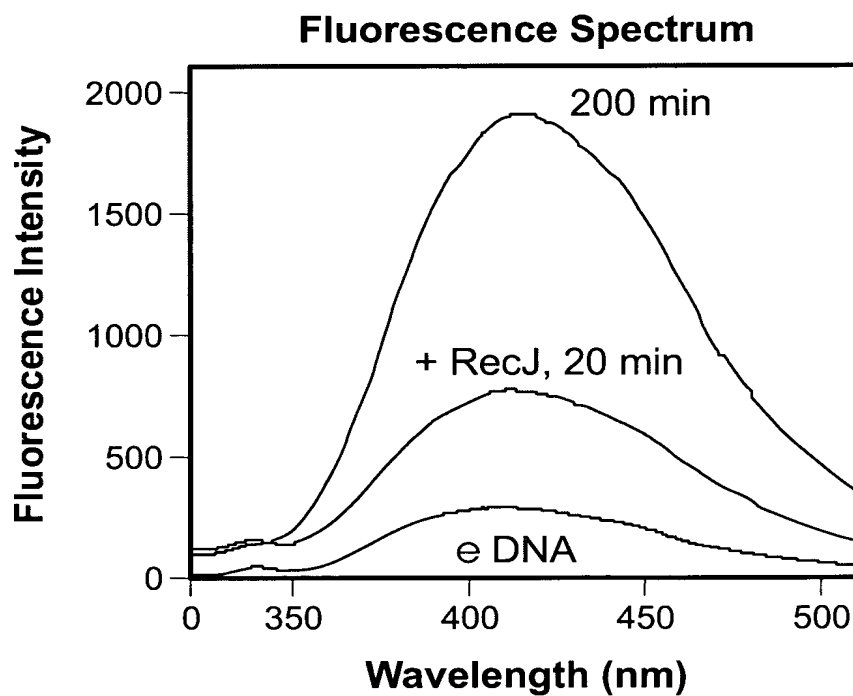
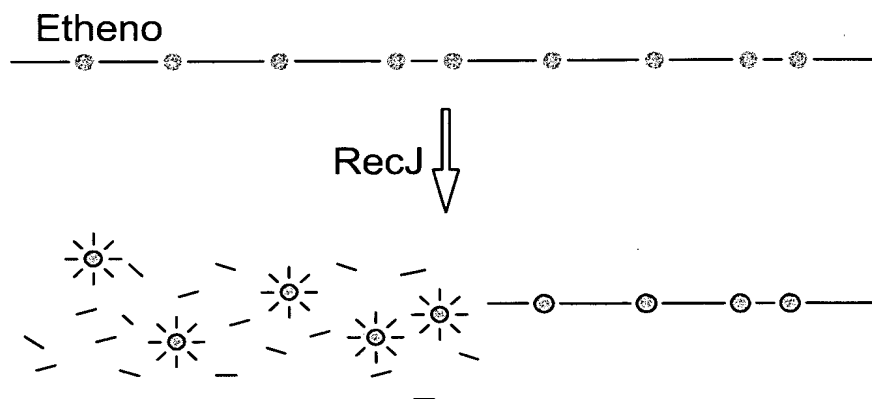


FIG. 21



20/36

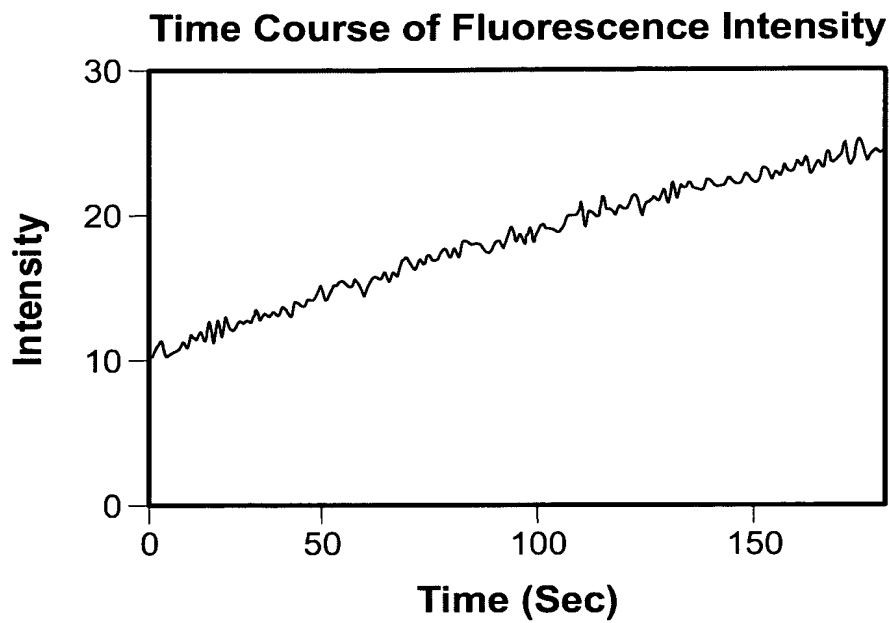


FIG. 22A

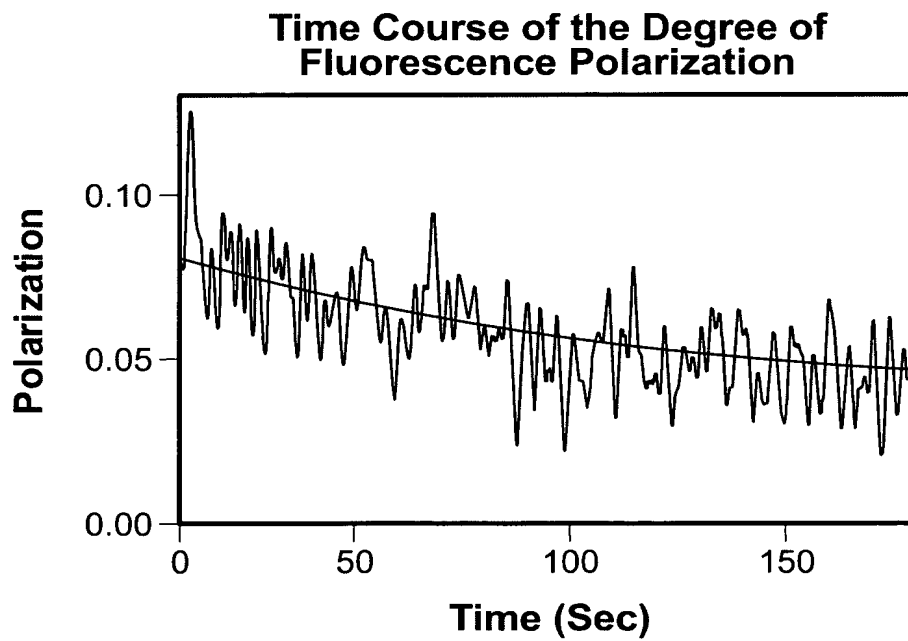


FIG. 22B



21/36

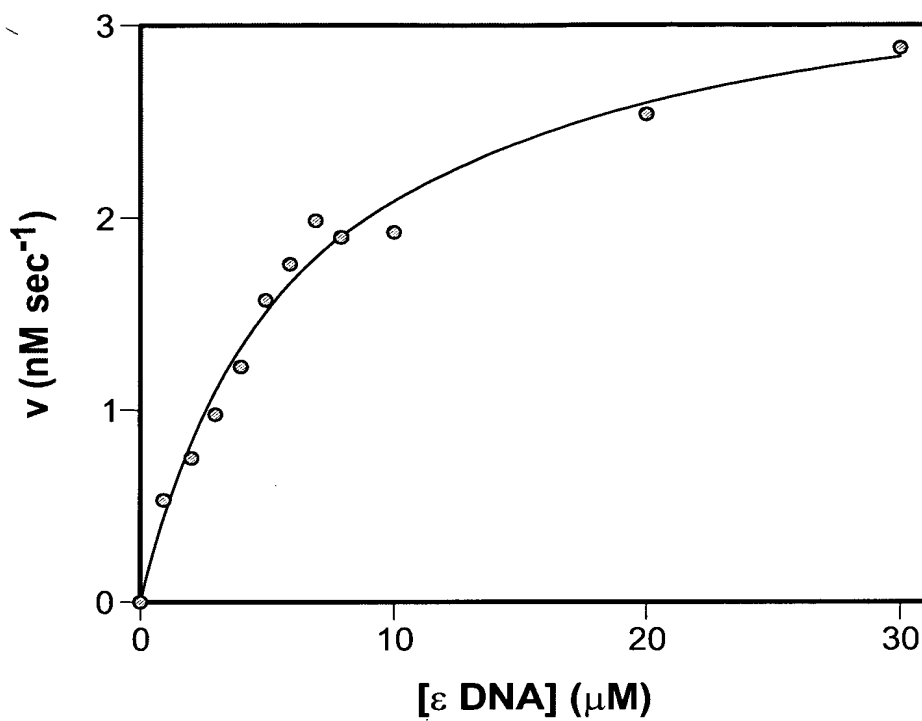
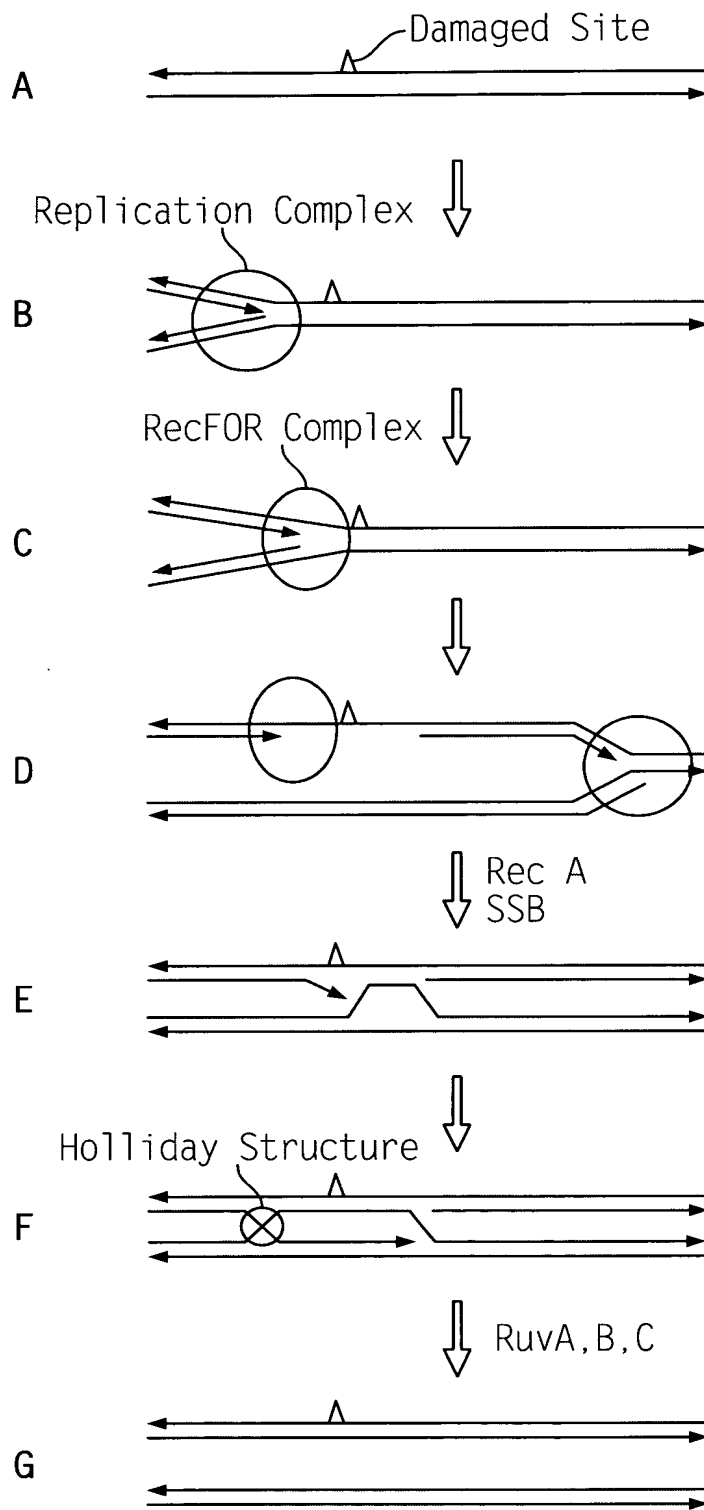


FIG. 23

**22/36****FIG. 24**



23/36

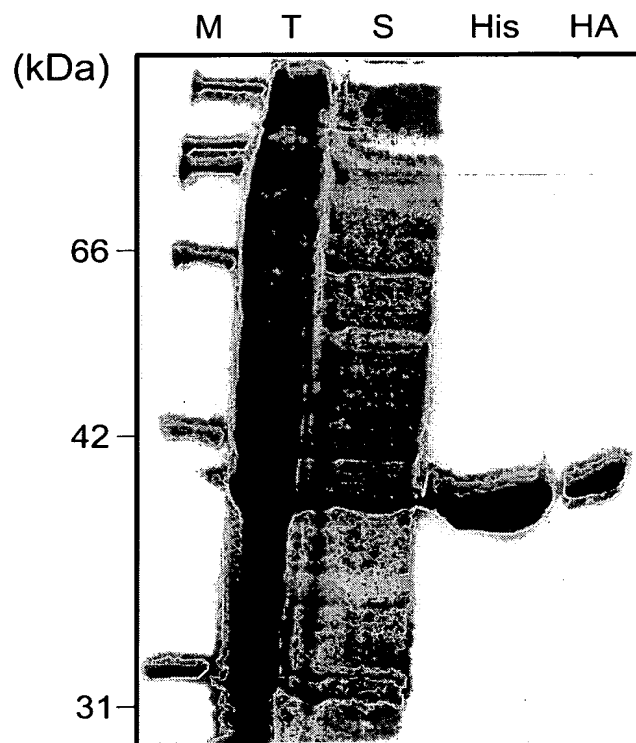


FIG. 25



24/36

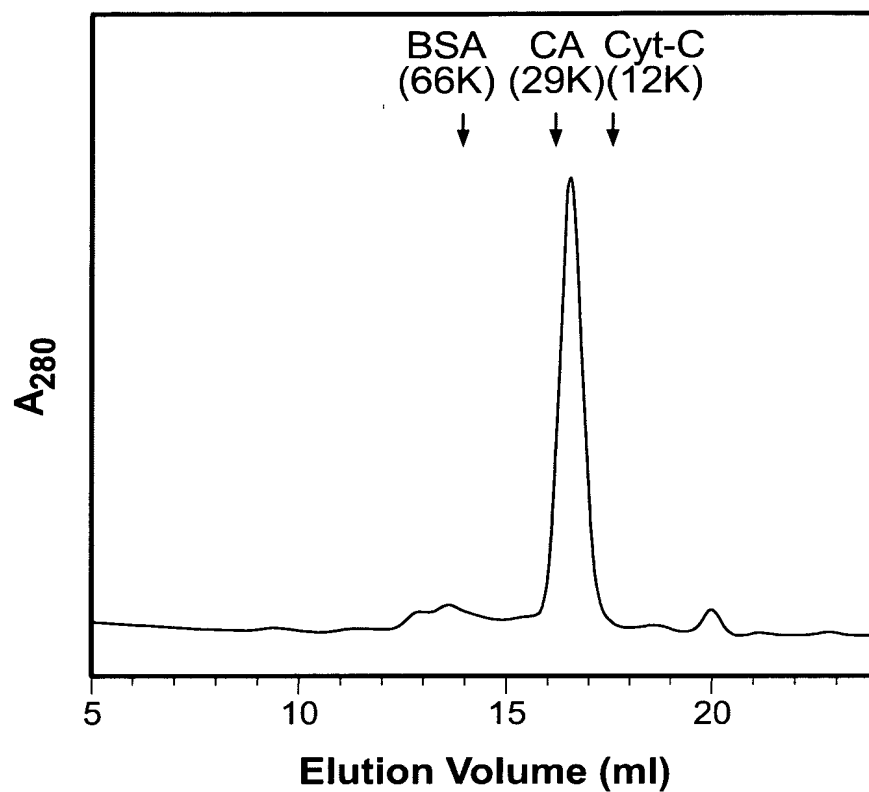


FIG. 26



26/36

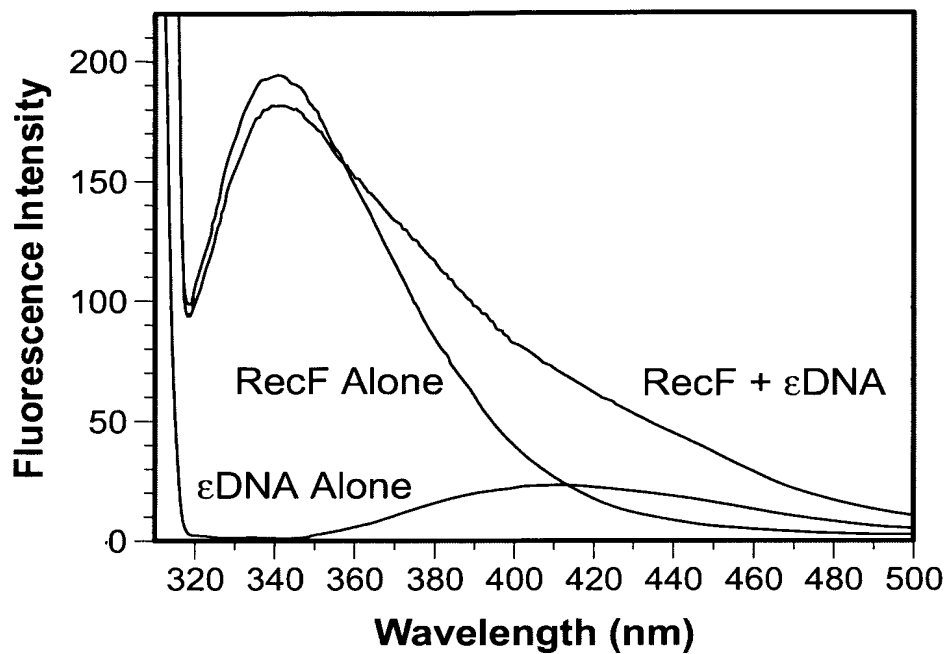


FIG. 28A

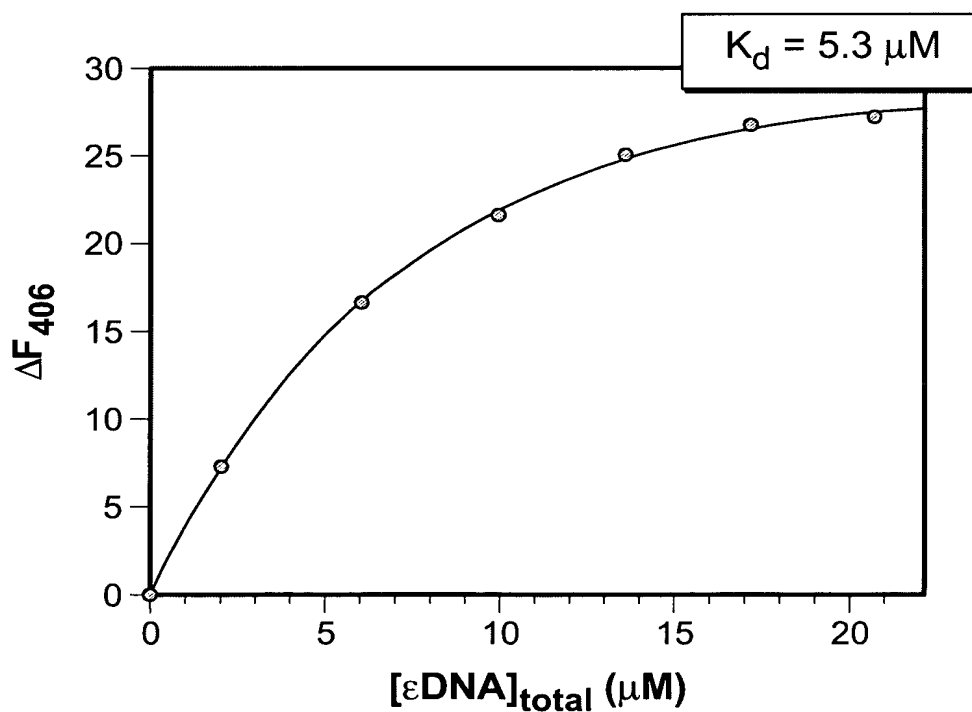


FIG. 28B



27/36

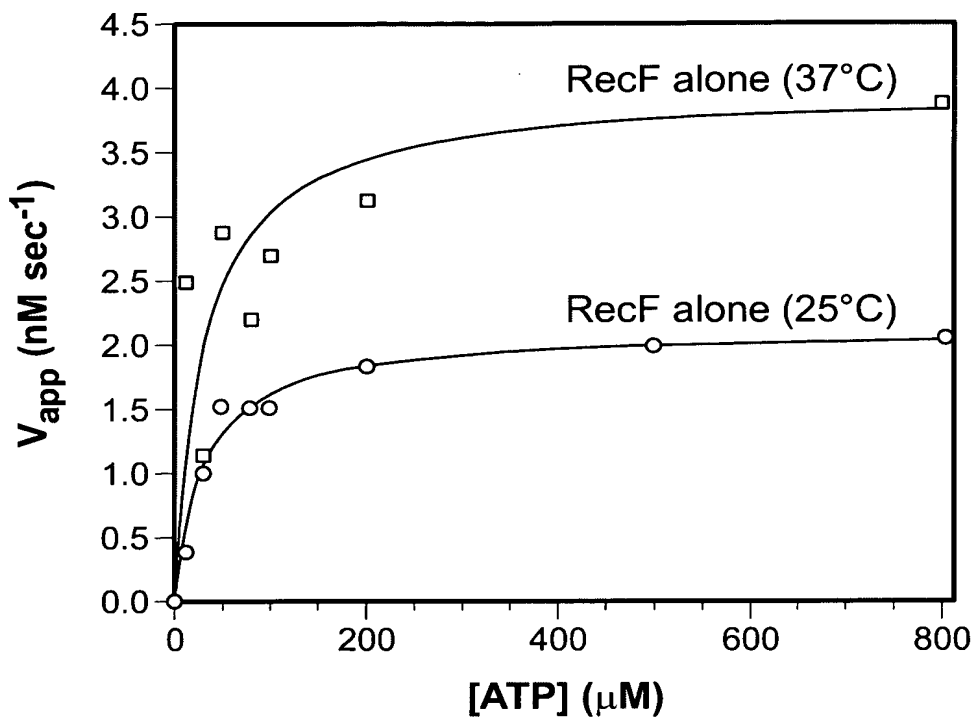


FIG. 29

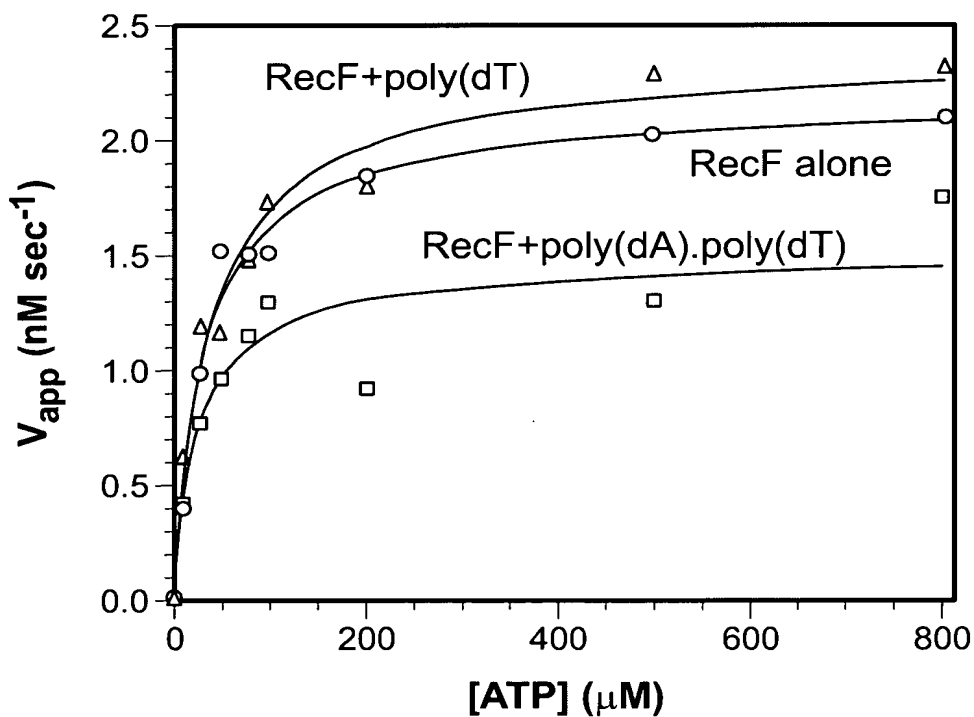


FIG. 30



28/36

Repair of Entire Genome

Transcription-Coupled
Repair

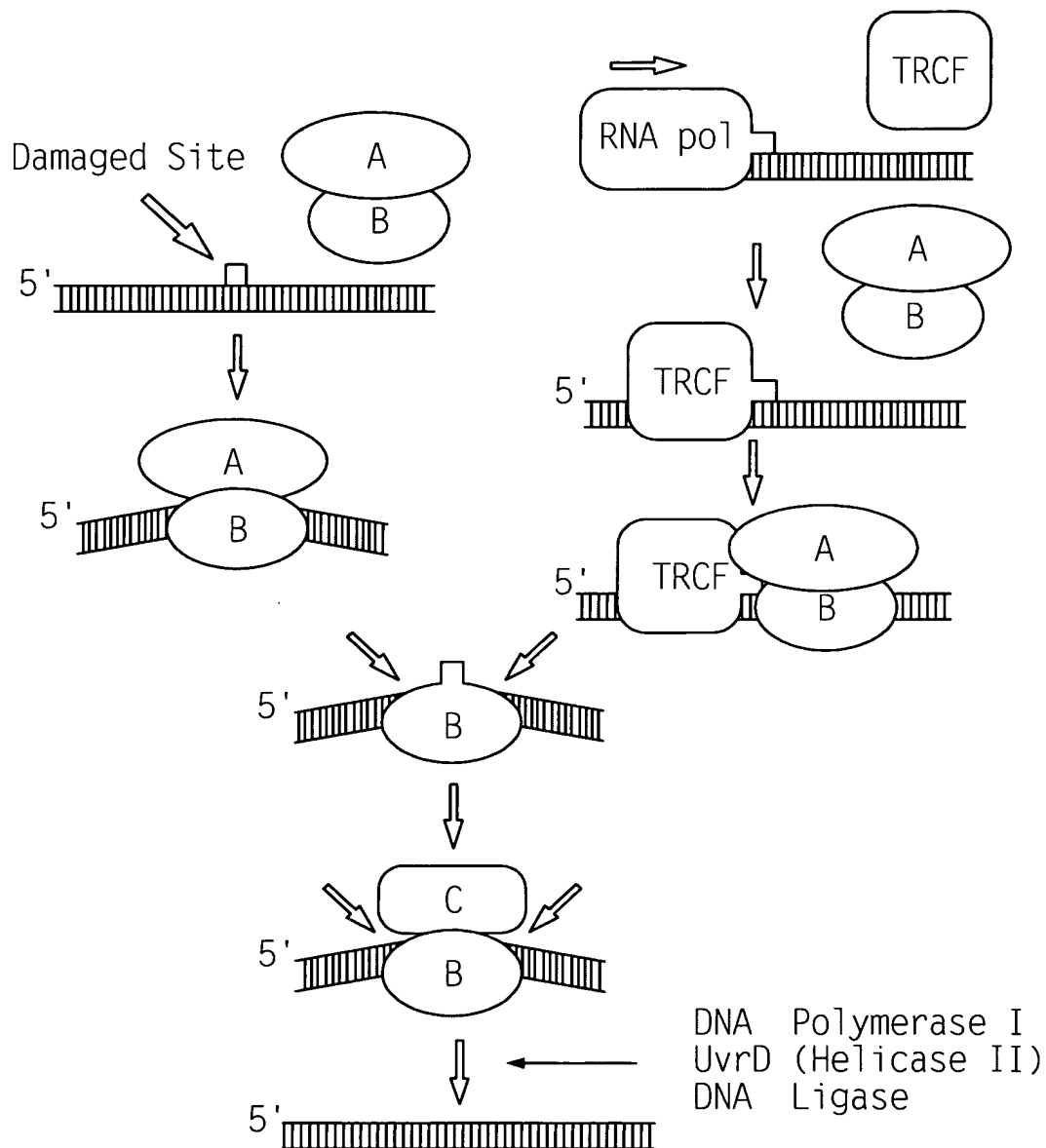


FIG. 31



29/36

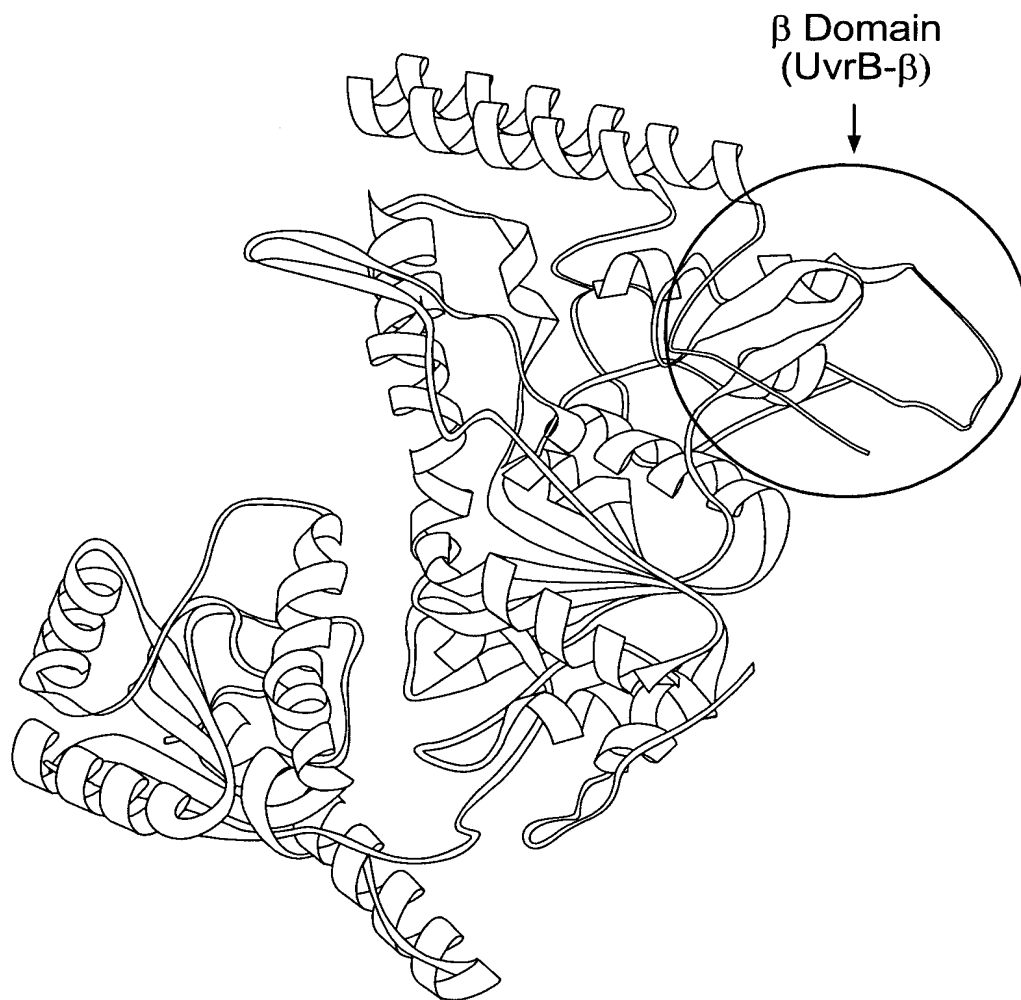


FIG. 32



Applicant(s): Kuramitsu, et al.

NOVEL DNA REPAIR ENZYMES, NUCLEIC ACIDS
ENCODING DNA REPAIR ENZYMES AND METHODS OF
USING THEM

30/36

UvrB- β

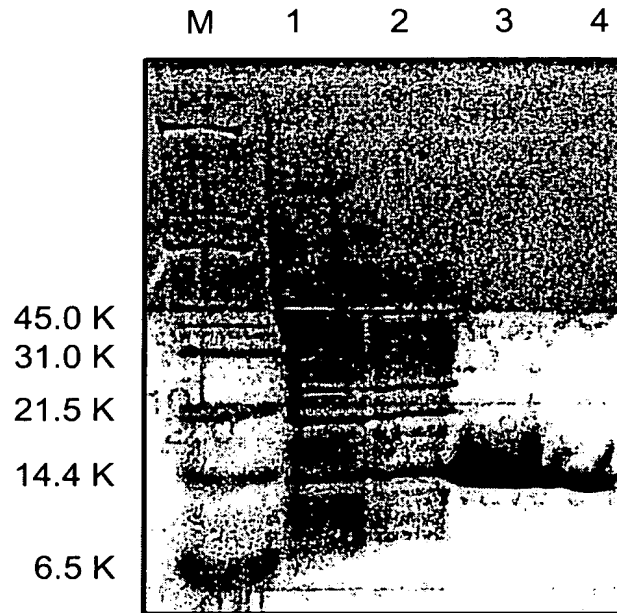


FIG. 33A

TRCF- β

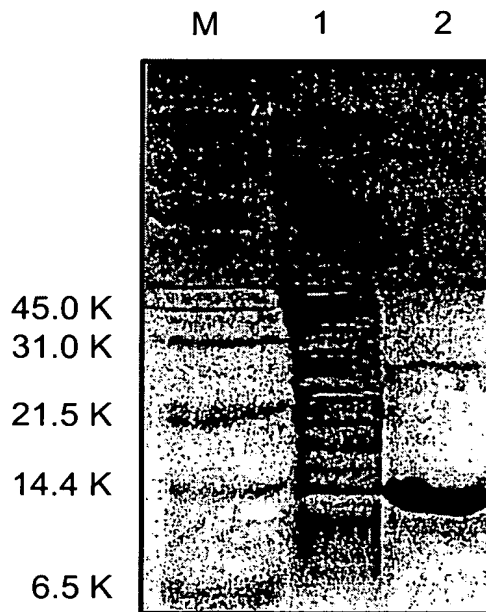


FIG. 33B



31/36

UvrB- β	154	RNLVVERGKPYPREVLLERLLELGYQRNDI	184
TRCF- β	86	WRLLLEVGGRAYPREALLSRLLKLGYAR---	113
		* * * * *	

UvrB- β	185	DLSPGRFRKGEVLEIFPAYETETIRVELF	215
TRCF- β	114	DED---YRVLGEVVELG-----EVRLEFF	148
		* * * * *	

UvrB- β	216	GDEVERISQVHPVTG-ERLRELPG-----	236
TRCF- β	149	GDELERLVVRGEERRRHVLLPKPGKAEGFT	163
		* * * * *	

UvrB- β	237	---FVLFPA	242	*Identical Amino Acid Residues
TRCF- β	164	SKKVLHEPG	172	.Homologous Amino Acid Residues
		**		

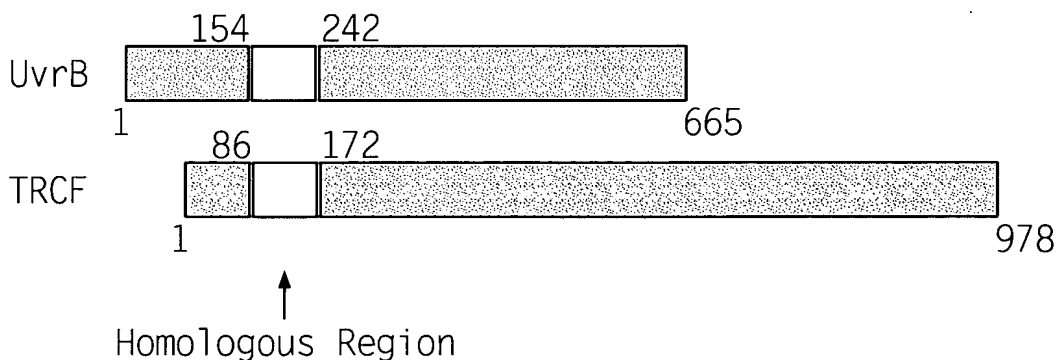
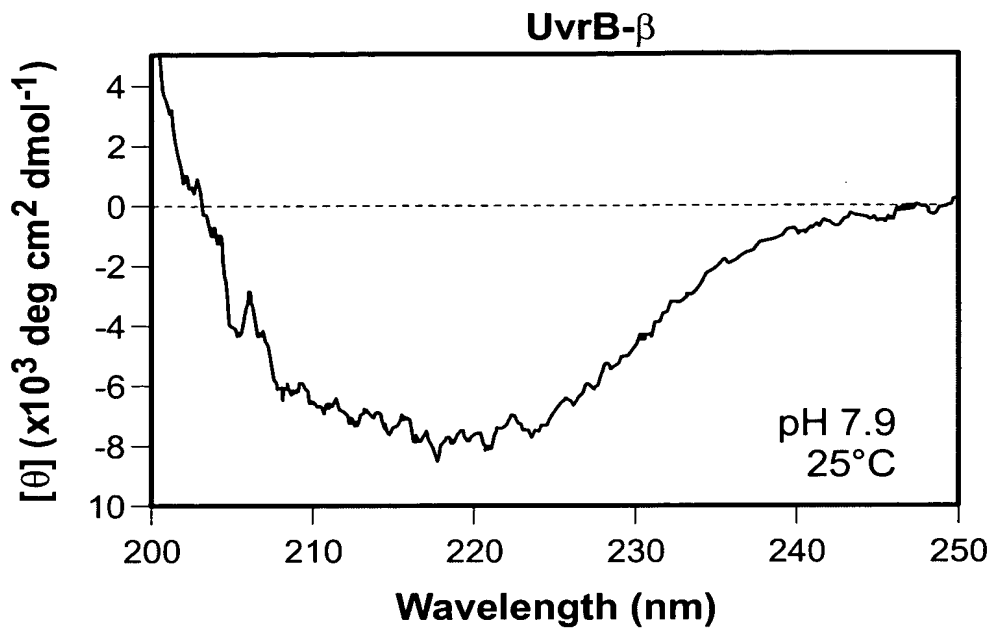
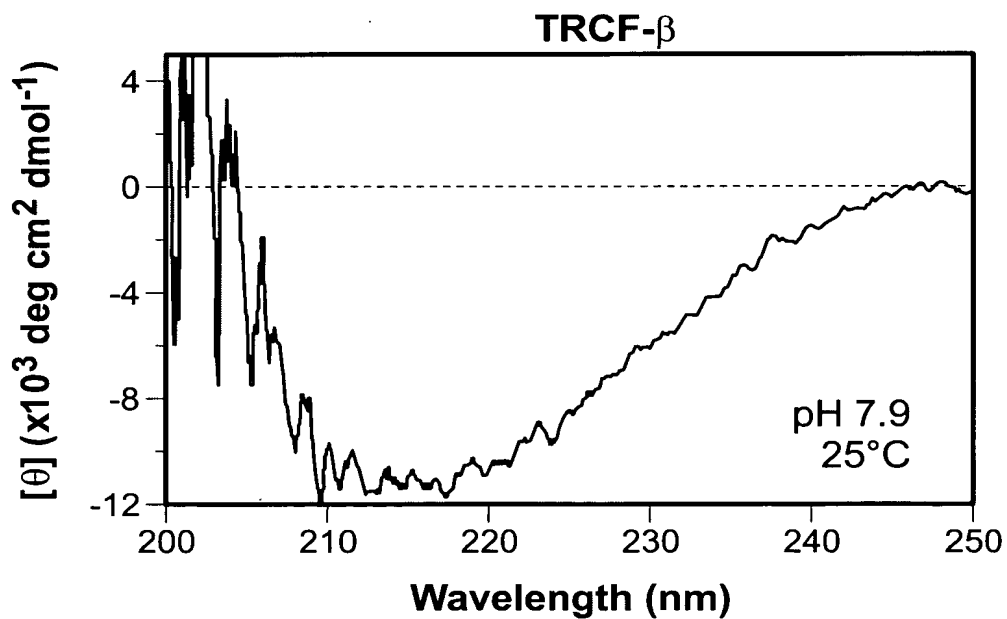


FIG. 34

**32/36****FIG. 35A****FIG. 35B**



33/36

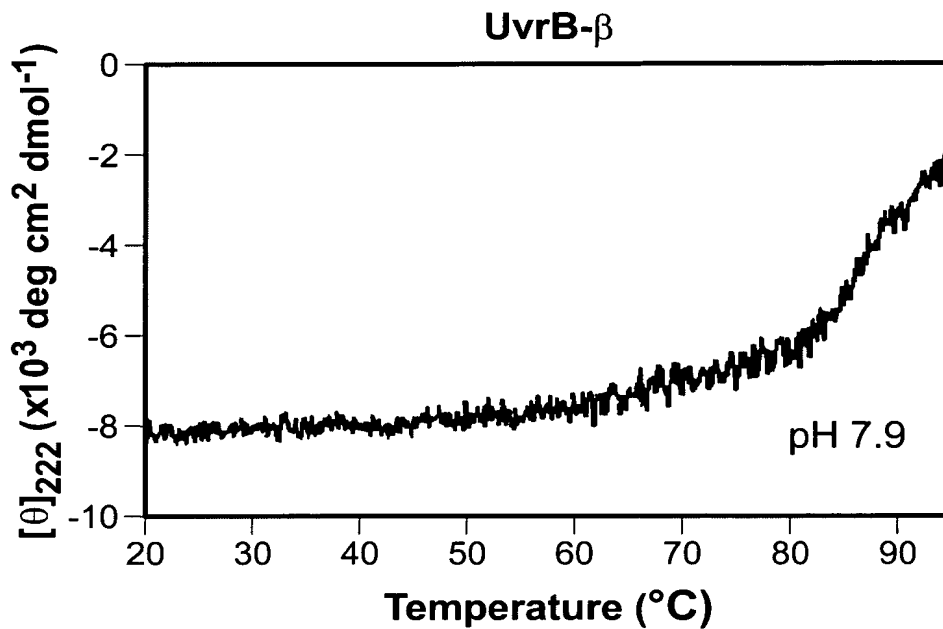


FIG. 36A

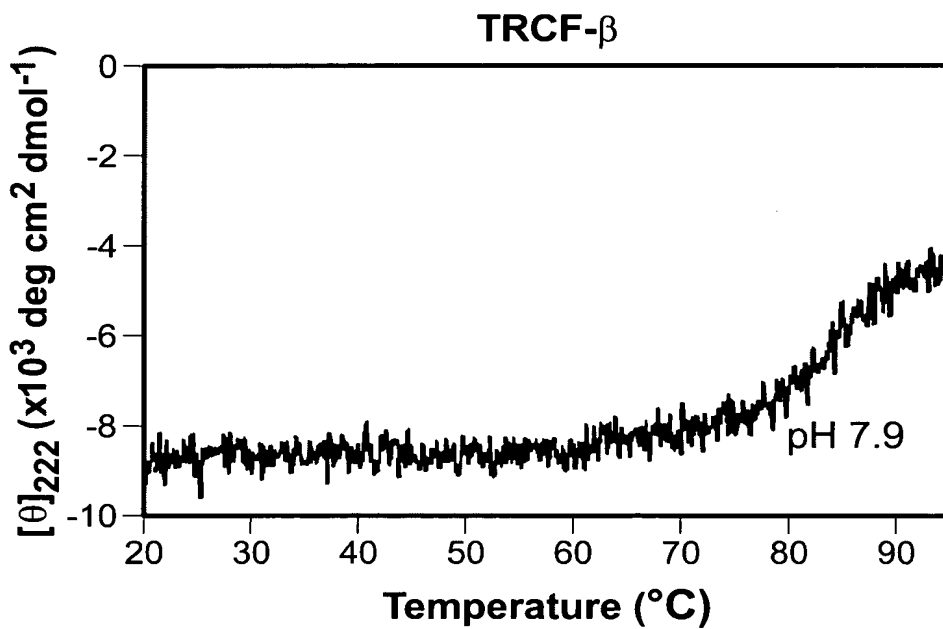


FIG. 36B



34/36

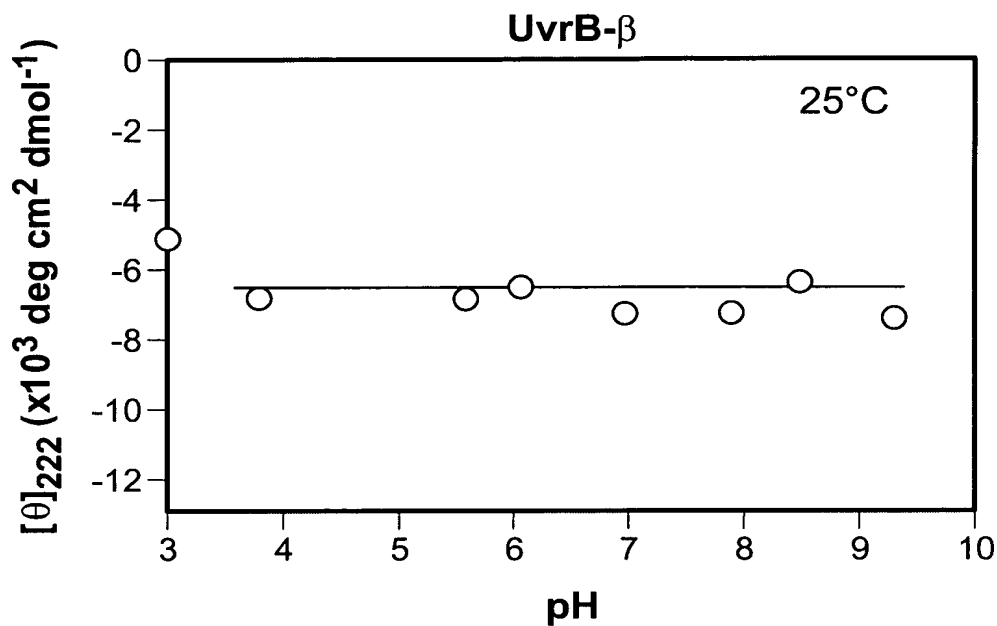


FIG. 37A

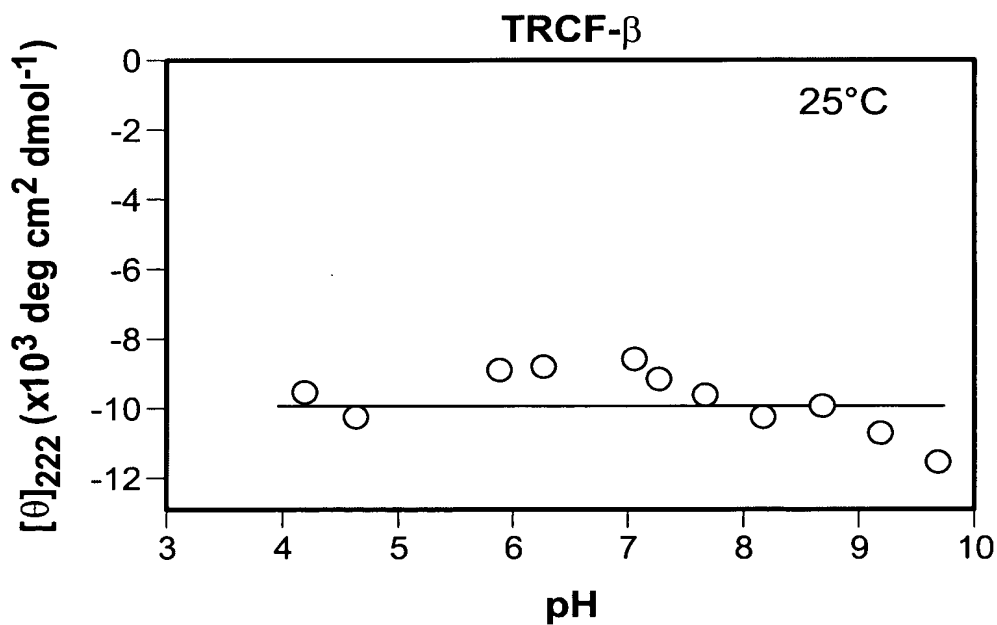


FIG. 37B



35/36

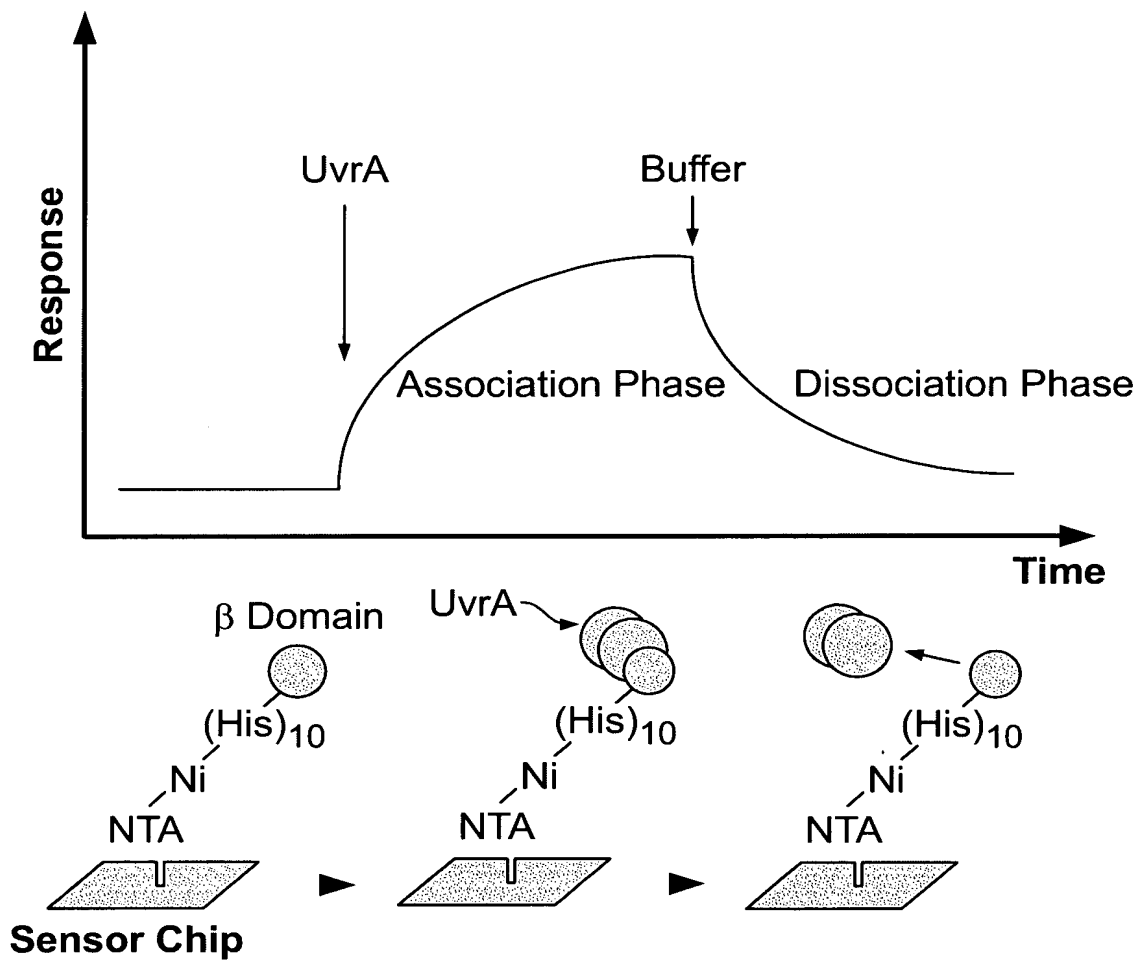
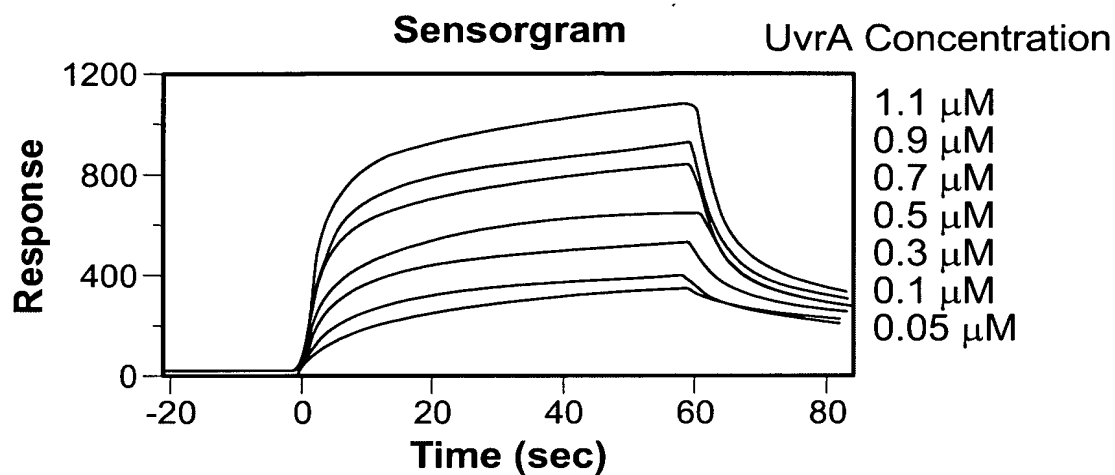


FIG. 38



36/36



Analytical Results

	K_d ($\times 10^{-6}M$)		k_{on} ($\times 10^5 M^{-1}S^{-1}$)		k_{off} ($\times 10^{-1}S^{-1}$)	
	-ATP	+ATP	-ATP	+ATP	-ATP	+ATP
UvrB-b	2.6	0.4	2.0	1.5	5.2	0.6
TRCF-b	1.3	0.5	1.0	1.5	1.3	0.7

FIG. 39

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☒ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.